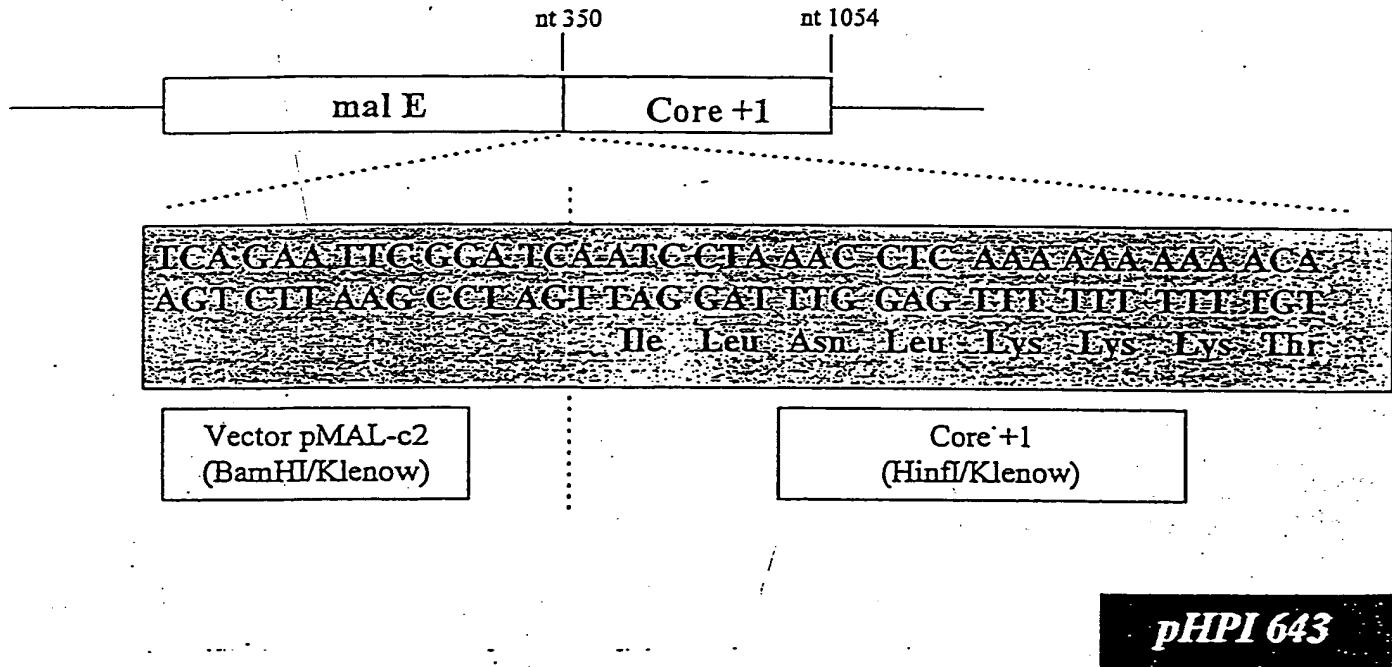


MalE-CORE+1 RECOMBINANT PROTEINS

A



B

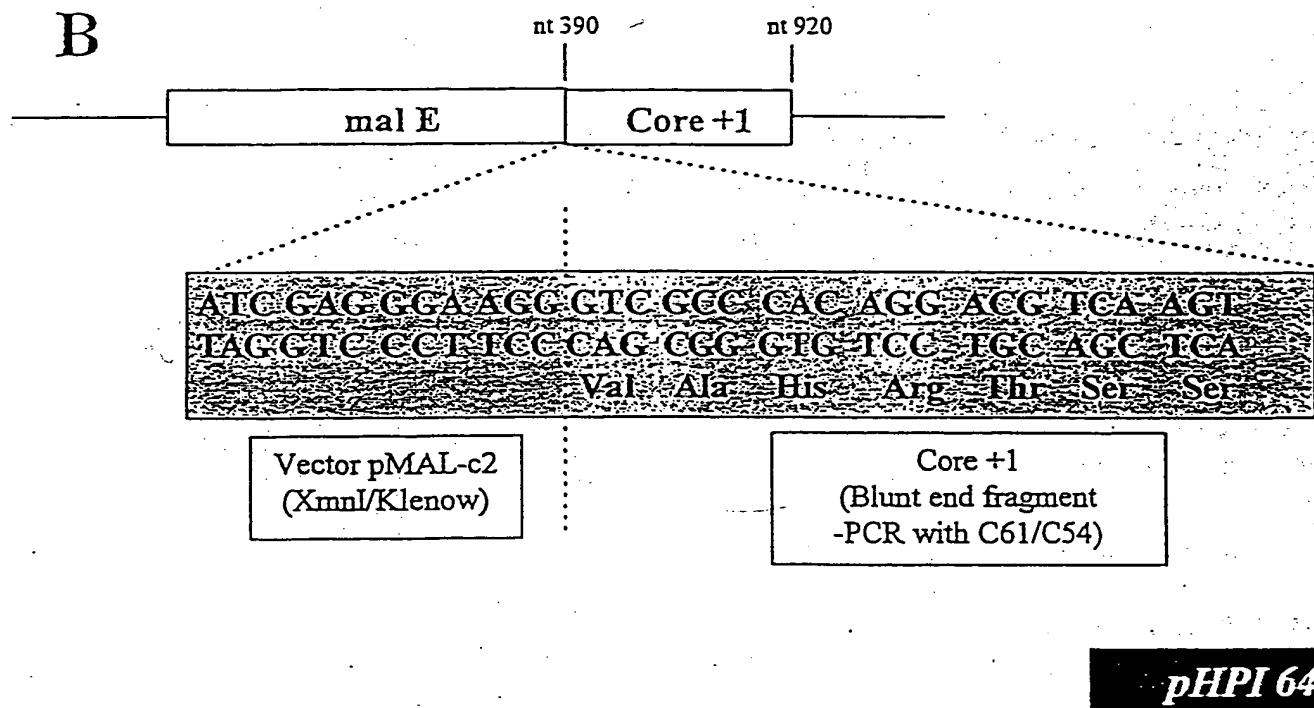
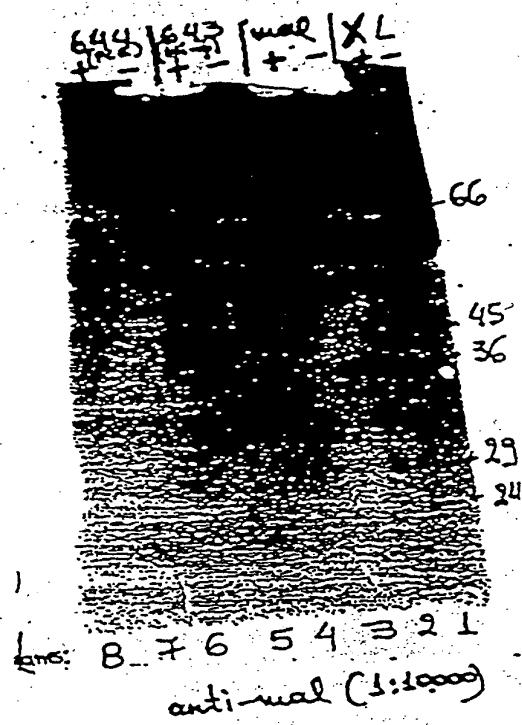


FIGURE 1

Panel A



Panel B

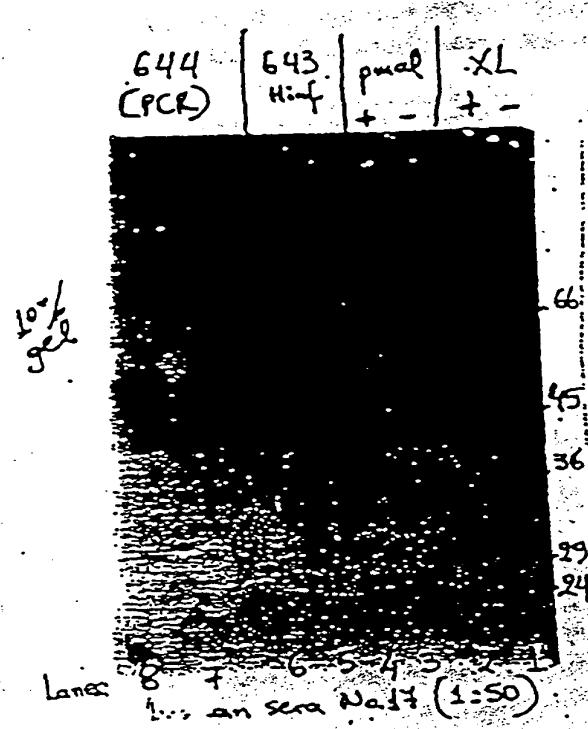


Figure 2

Panel A

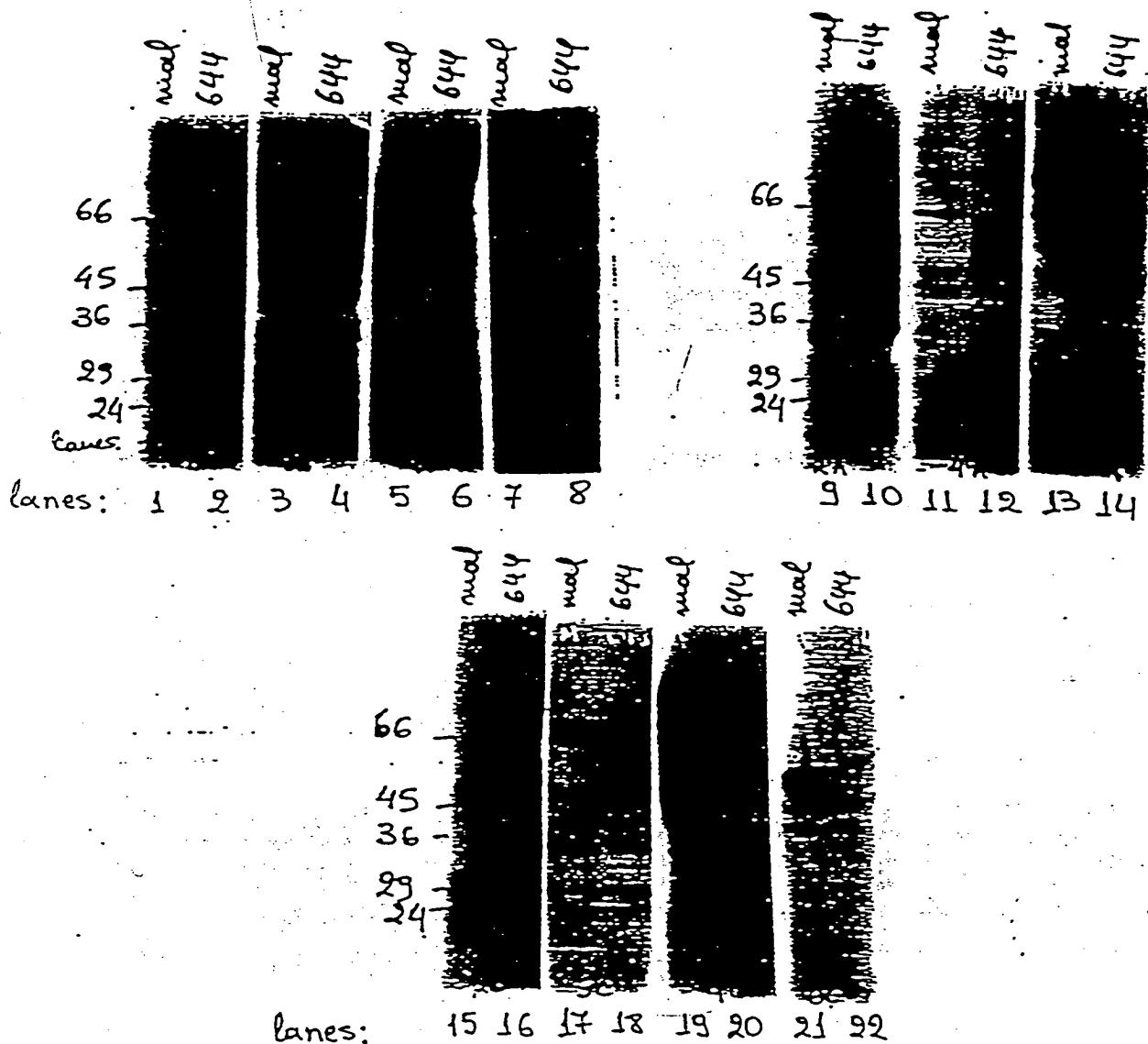


Figure 3

Panel B

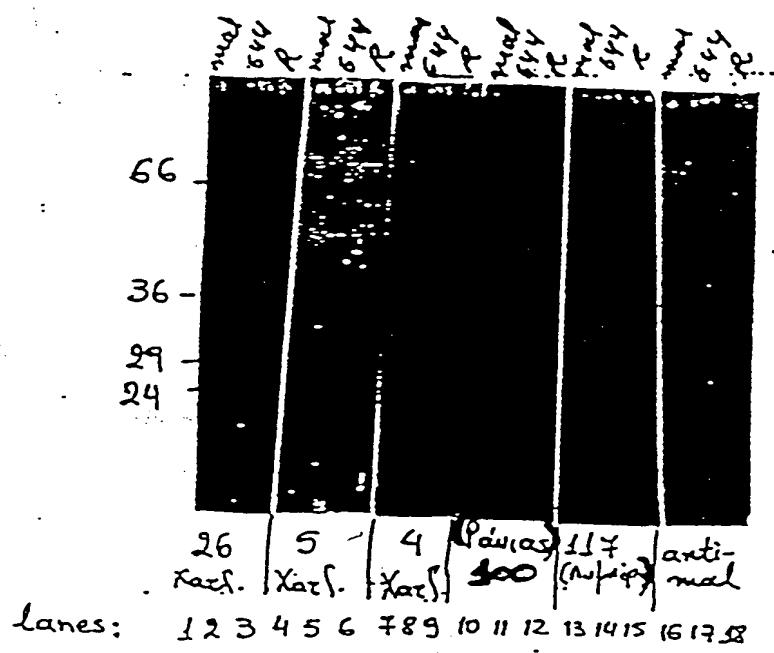
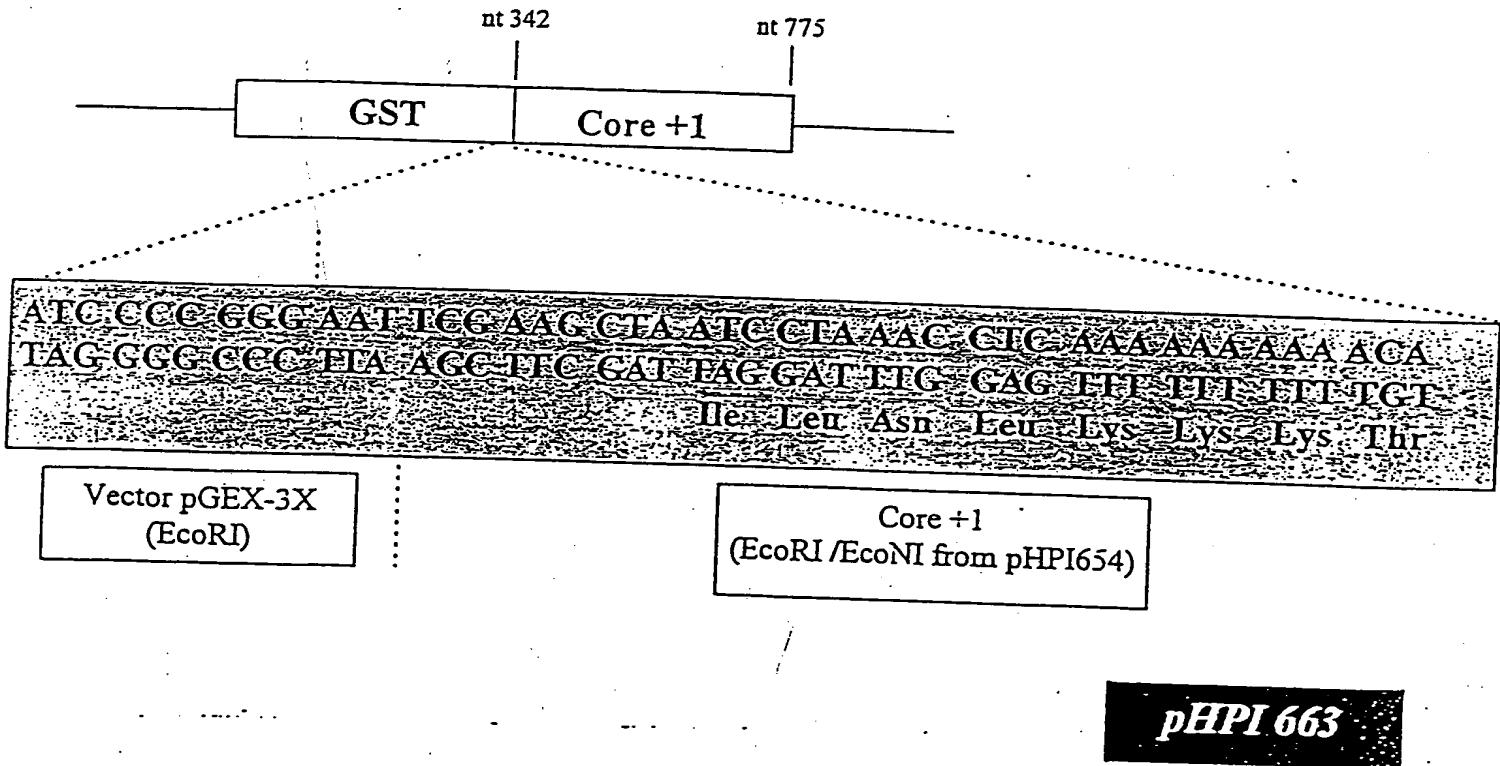


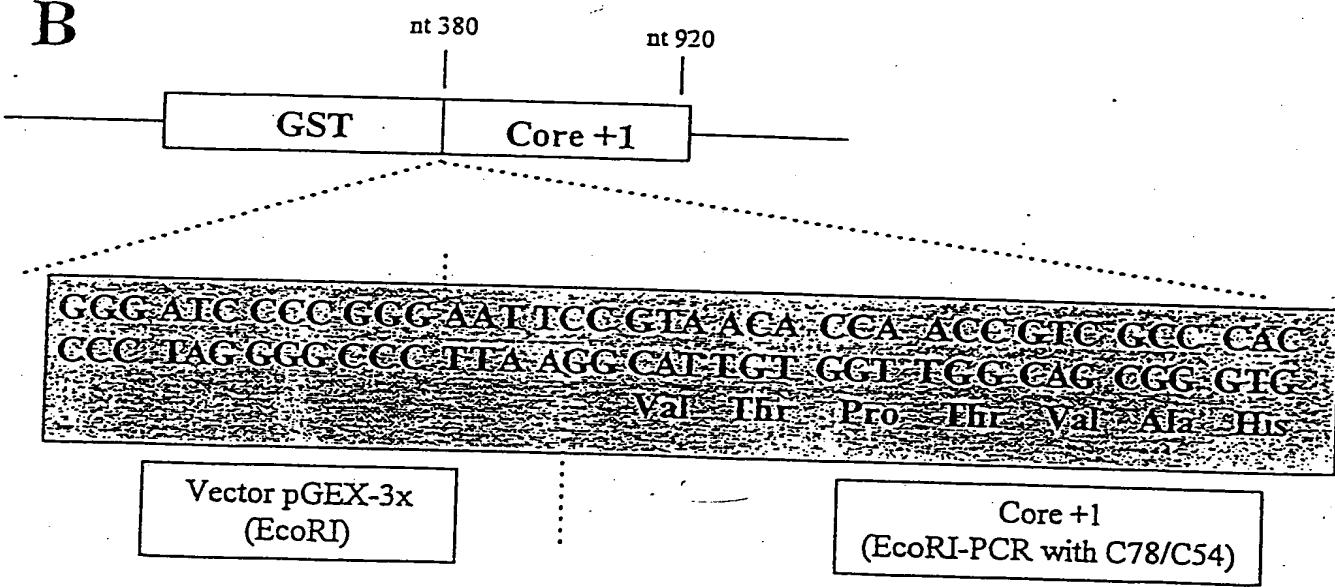
Figure 3 (cont.)

GST-CORE+1 RECOMBINANT PROTEINS

A



B



pHPI 668

FIGURE 4

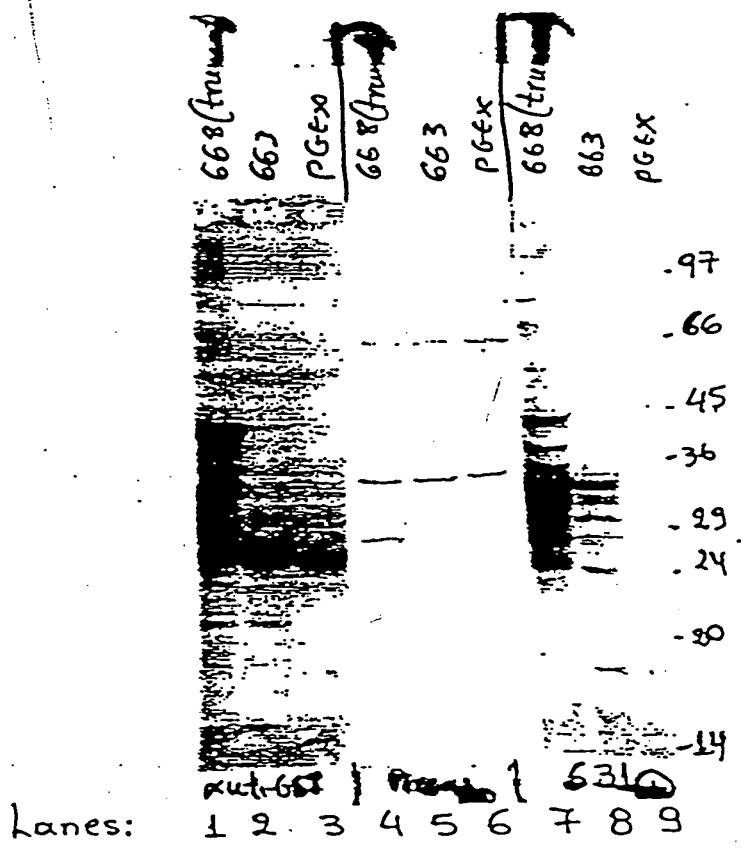


Figure 5

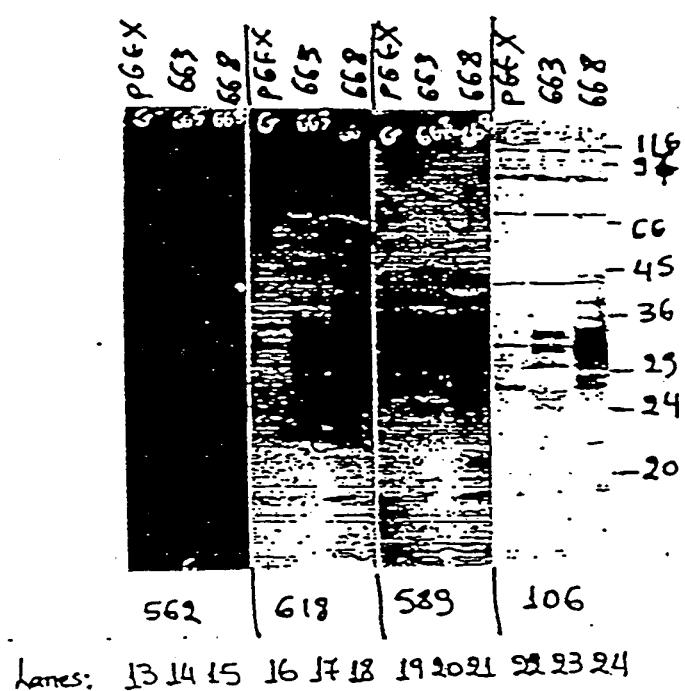
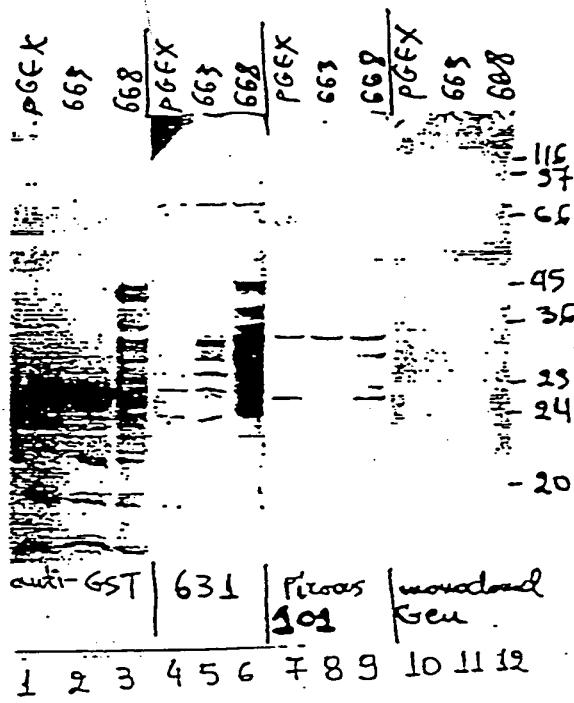
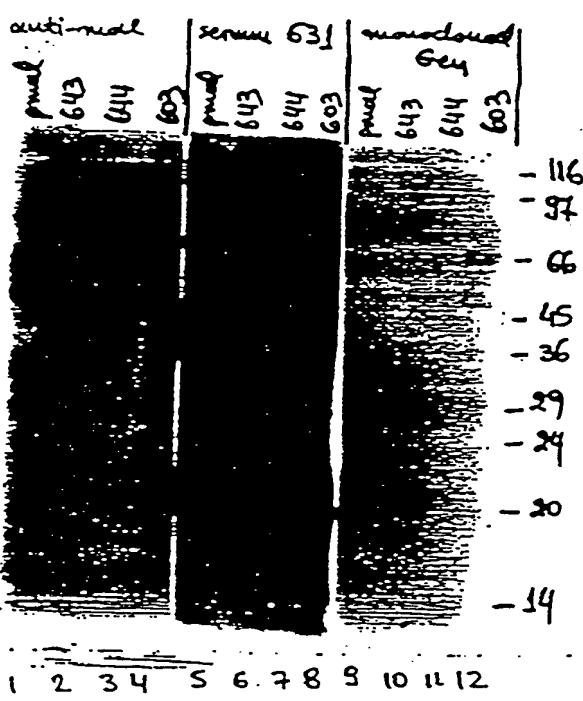


Figure 6

Panel A



ECL detected

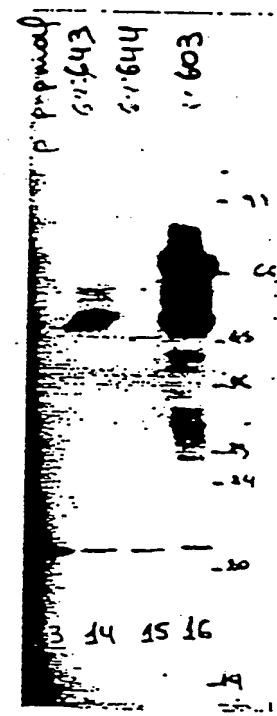
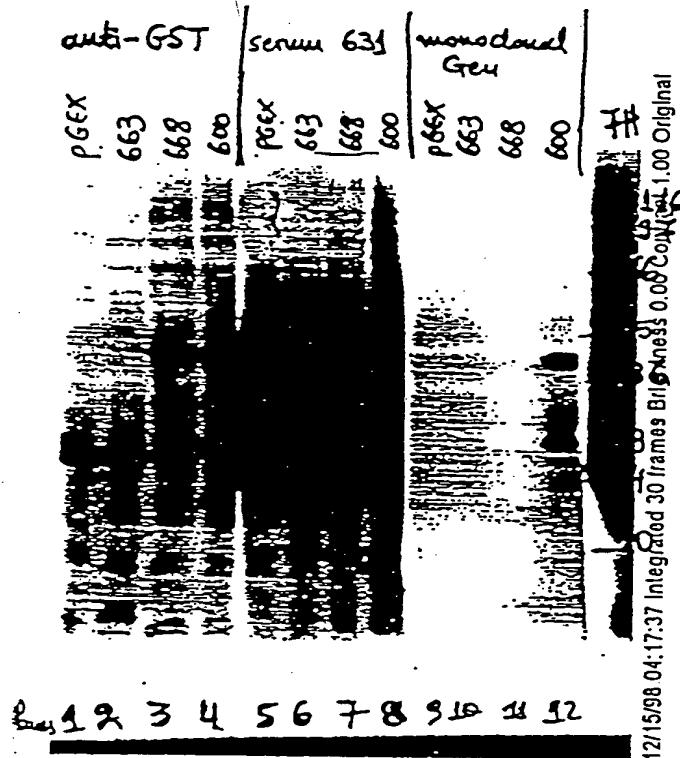


Figure 7

Panel B



lanes: 13 14 15 16

Figure 7 (Cont.)

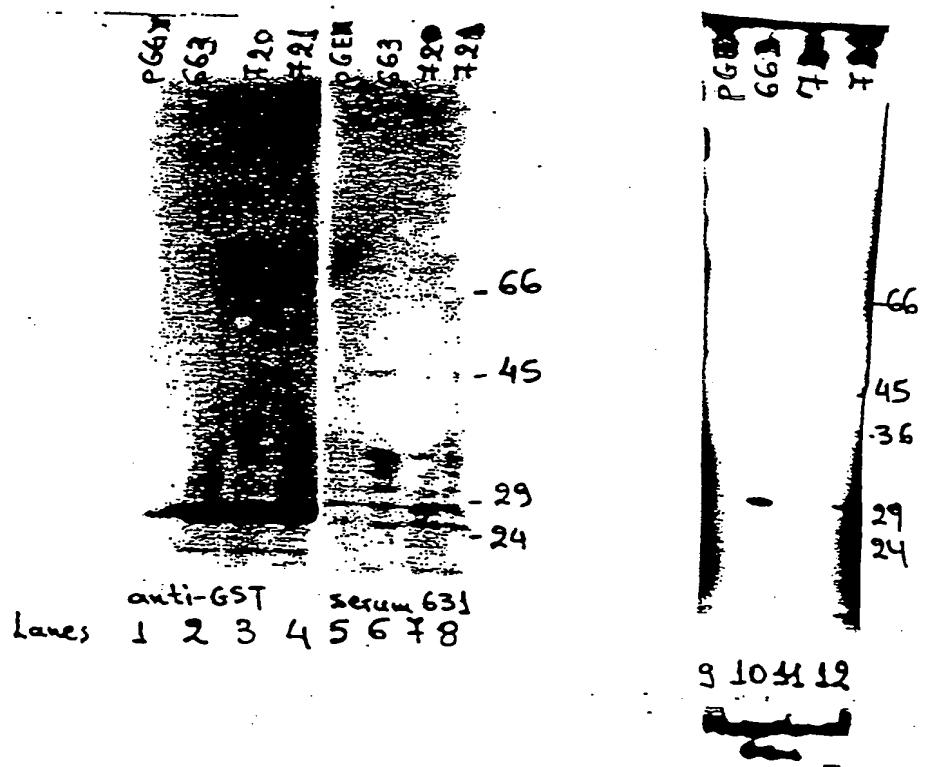


Figure 8

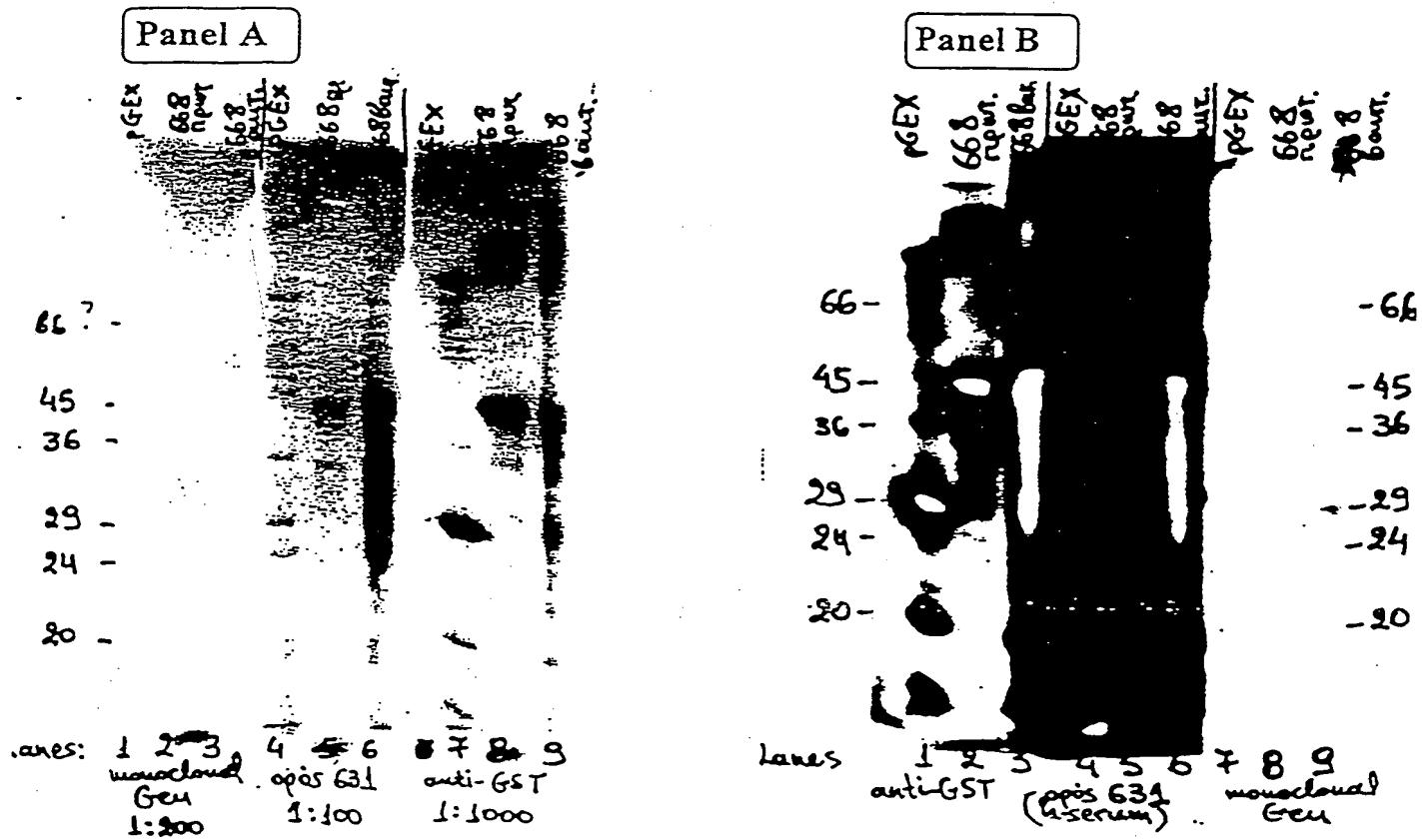


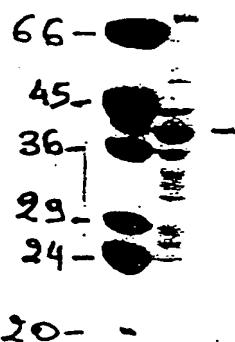
Figure 9

Panel C

Coomassie staining

M 668 Baur.
BB input.
rEX

24



Lanes: 1 2 3 4

Figure 9 (cont.)

by D. Stewart and M. ...
Washington University

Wild type
pHPI 643 &
pHPI 663

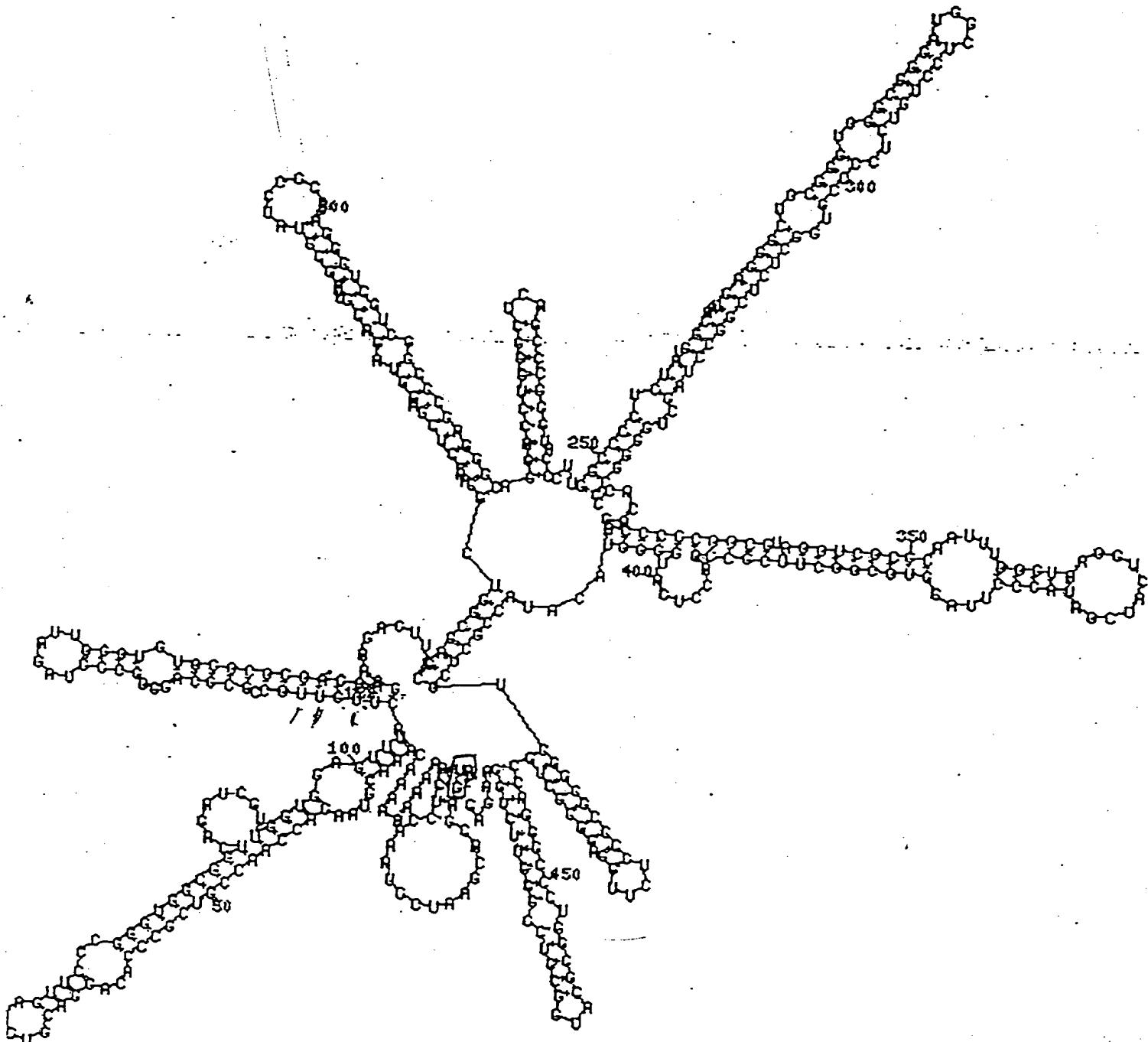


Figure 10 a

f by D. Stewart and M. Zuker
Washington University

His → Leu
pHPI 676

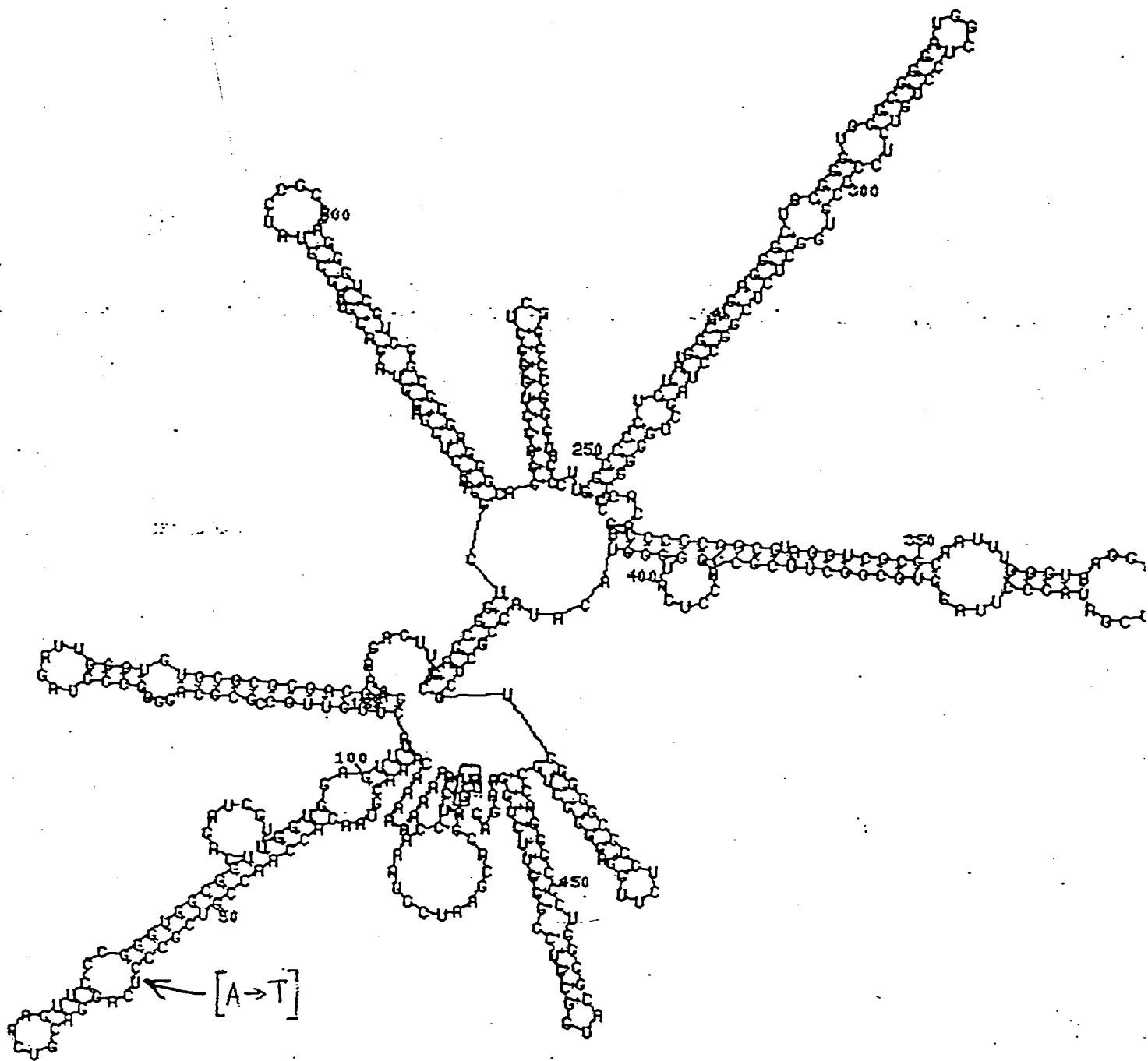


Figure 10 b

by D. Stewart and M. Zuker
Washington University

Cys → Ser
pHPI 679

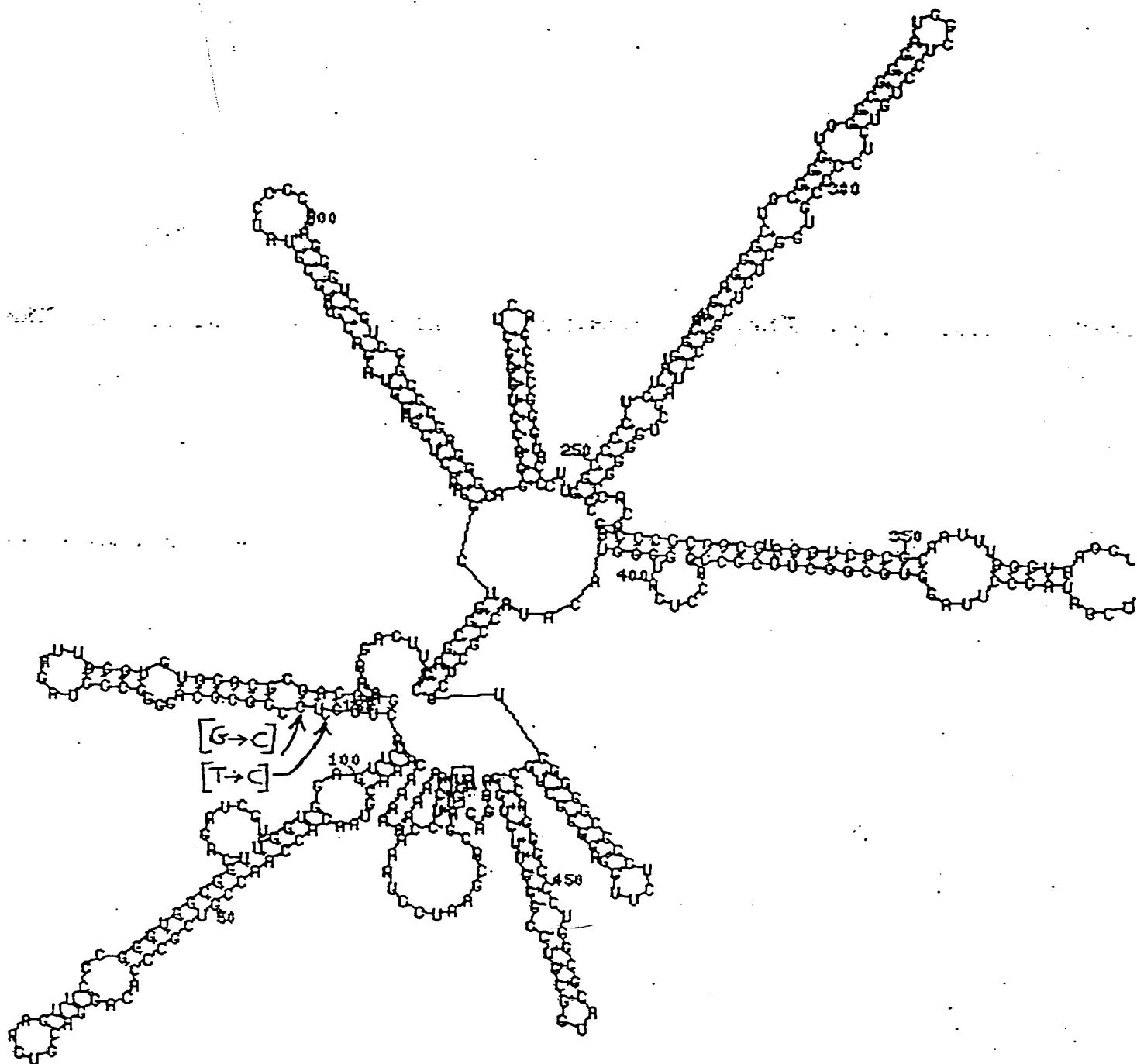


Figure 10 c

D. Stewart and M. Zuker
ington University

His \rightarrow Leu & Cys \rightarrow Ser
pHPI 719

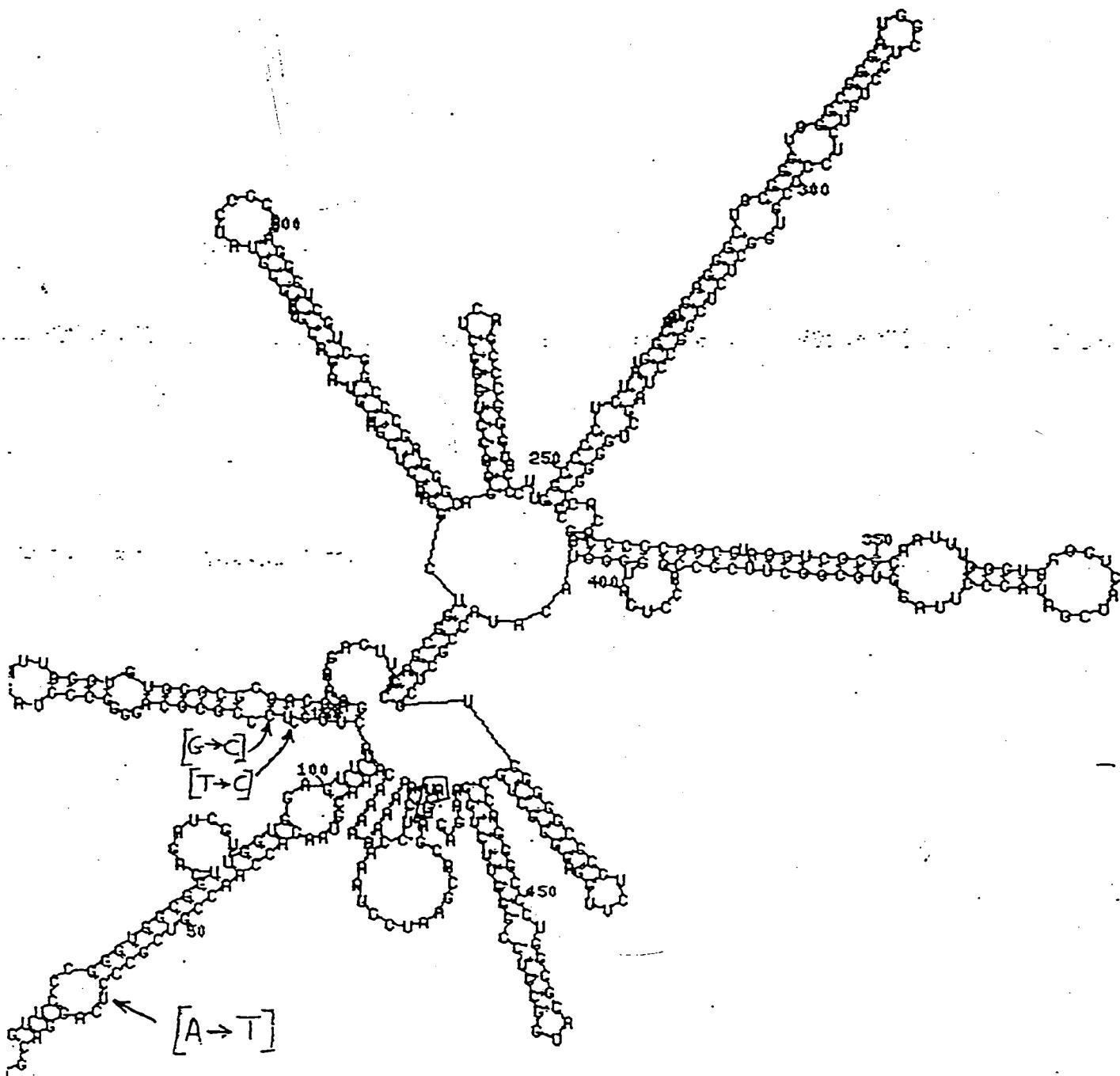


Figure 10 d

by D. Stewart and M. ...
Washington University

Cys-Cys → Gly-Gly
pHPI 720

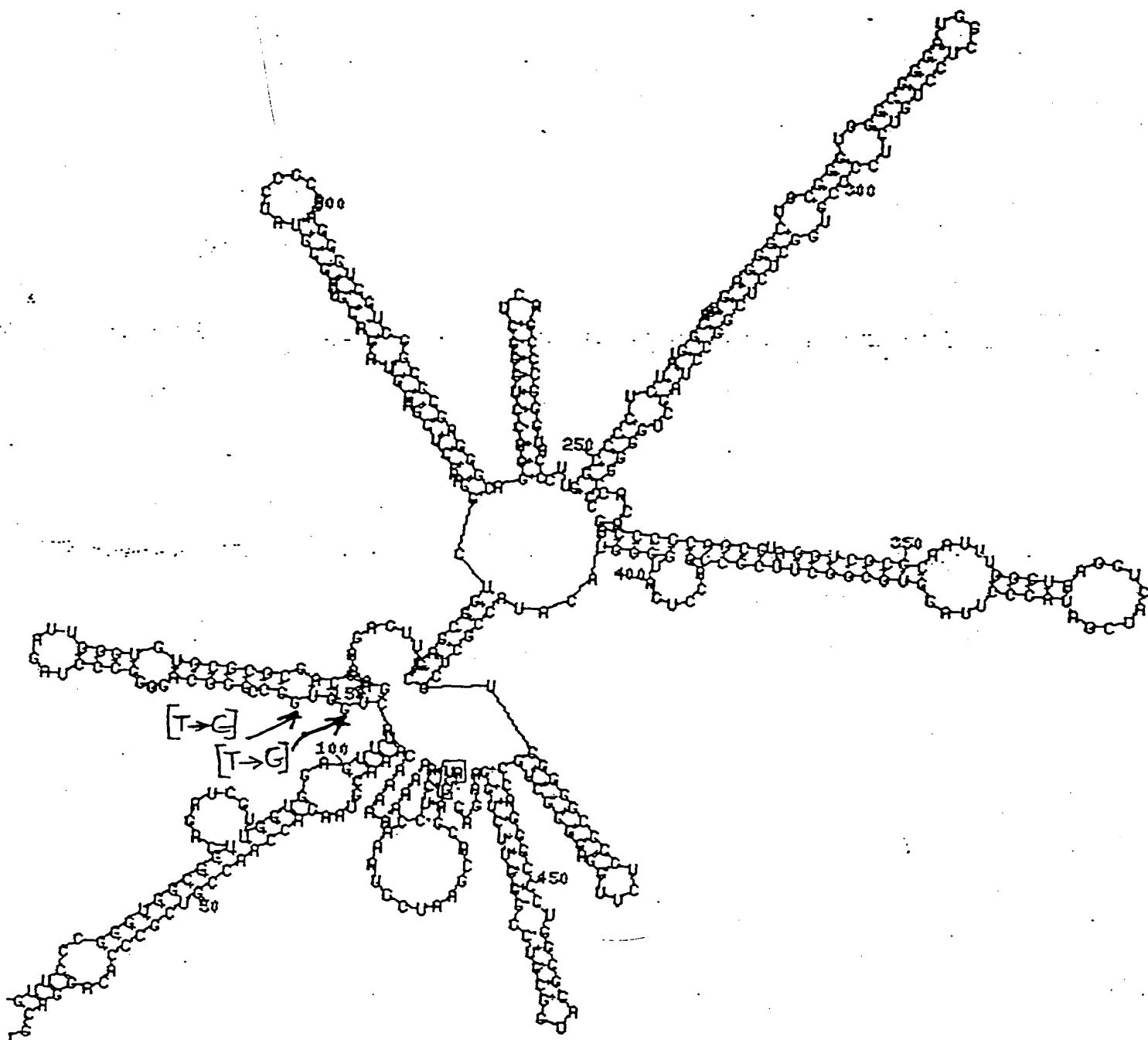
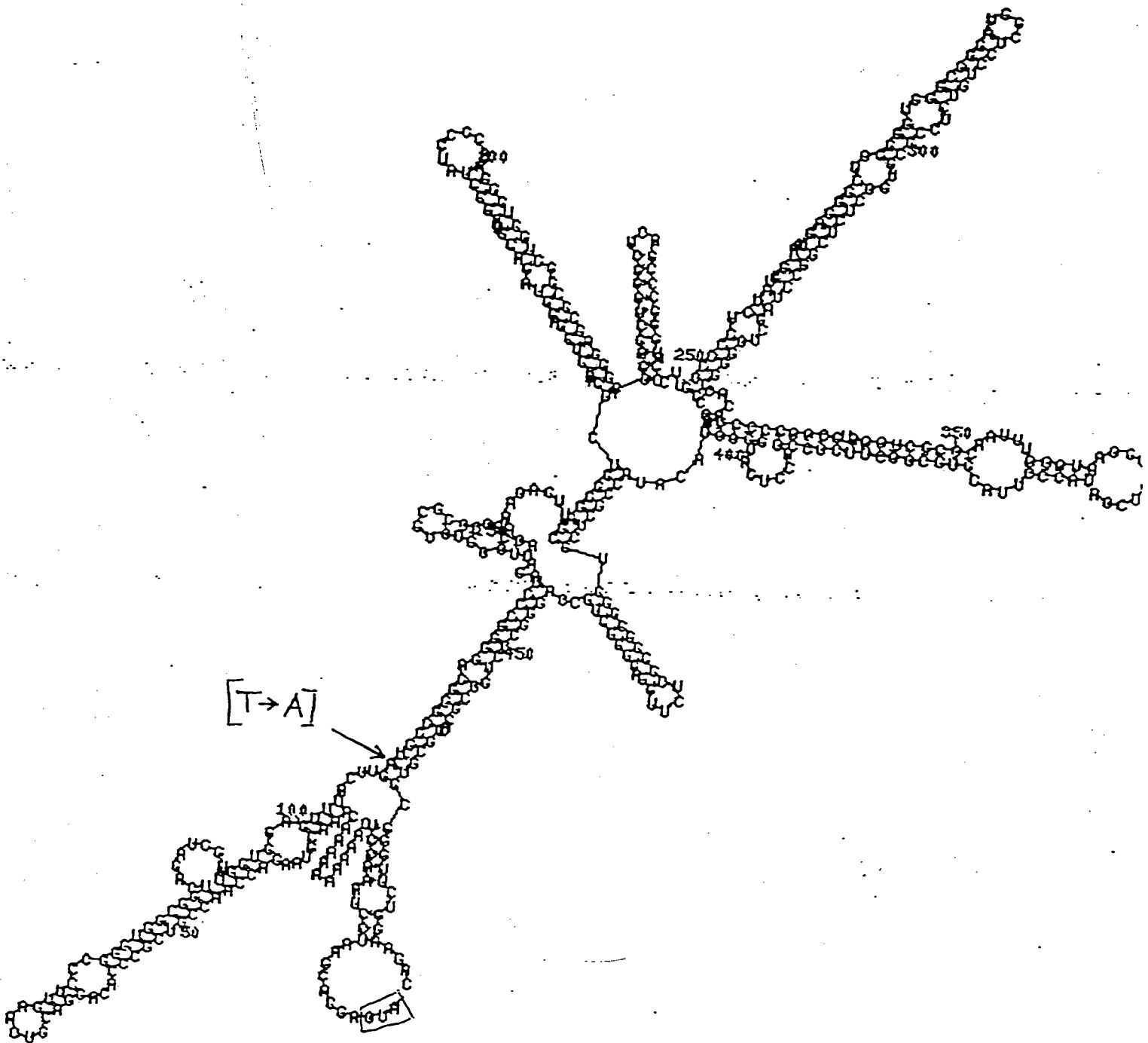


Figure 10 e

Cys → stop codon
pHPI 721



ENERGY = -236.1 [initial] 0.000000

Figure 10f

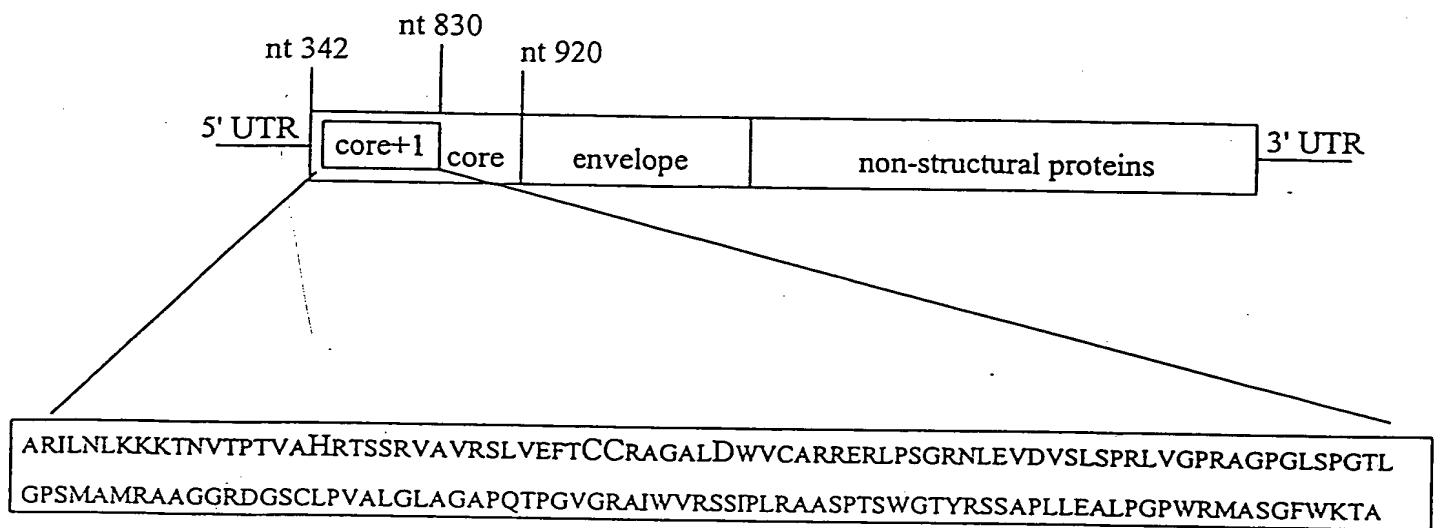


FIG. 11

Sequence Range: 342 to 840

350 360 370 380 390

A TGA GCA CGA ATC CTA AAC CTC AAA AAA AAA ACA AAC GTA ACA CCA ACC
 T ACT CGT GCT TAG GAT TTG GAG TTT TTT TTT TGT TTG CAT TGT GGT TGG
 *** Ala Arg Ile Leu Asn Leu Lys Lys Lys Thr Asn Val Thr Pro Thr>
 _a_a_ TRANSLATION OF HCVSEND.SEQ (RITS) [A]_a_a_a_>

400 410 ^{Purine} 420 430

GTC GCC CAC AGG ACG TCA AGT TCC CGG GTG GCG GTC AGA TCG TTG GTG
 CAG CGG GTG TCC TGC AGT TCA AGG GCC CAC CGC CAG TCT AGC AAC CAC
 Val Ala His Arg Thr Ser Ser Arg Val Ala Val Arg Ser Leu Val>
 _a_a_ TRANSLATION OF HCVSEND.SEQ (RITS) [A]_a_a_a_>

440 450 460 470 480

GAG TTT ACT TGT TGC CGC GCA GGG GCC CTA GAT TGG GTG TGC GCG CGA
 CTC AAA TGA ACA ACG GCG CGT CCC CGG GAT CTA ACC CAC ACG CGC GCT
 Glu Phe Thr Cys Cys Arg Ala Gly Ala Leu Asp Trp Val Cys Ala Arg>
 _a_a_ TRANSLATION OF HCVSEND.SEQ (RITS) [A]_a_a_a_>

490 500 510 520 530

CGA GAA AGA CTT CCG AGC GGT CGC AAC CTC GAG GTA GAC GTC AGC CTA
 GCT CTT TCT GAA GGC TCG CCA GCG TTG GAG CTC CAT CTG CAG TCG GAT
 Arg Glu Arg Leu Pro Ser Gly Arg Asn Leu Glu Val Asp Val Ser Leu>
 _a_a_ TRANSLATION OF HCVSEND.SEQ (RITS) [A]_a_a_a_>

540 550 560 570 580

TCC CCA AGG CTC GTC GGC CCG AGG GCA GGA CCT GGG CTC AGC CCG GGT
 AGG GGT TCC GAG CAG CCG GGC TCC CGT CCT GGA CCC GAG TCG GGC CCA
 Ser Pro Arg Leu Val Gly Pro Arg Ala Gly Pro Gly Leu Ser Pro Gly>
 _a_a_ TRANSLATION OF HCVSEND.SEQ (RITS) [A]_a_a_a_>

590 600 610 620 630

ACC CTT GGC CCC TCT ATG GCA ATG AGG CCT GCG GGT GGG CGG GAT GGC
 TGG GAA CCG GGG AGA TAC CGT TAC TCC CCA CGC CCA CCC GGC CTA CCG
 Thr Leu Gly Pro Ser Met Ala Met Arg Ala Ala Gly Gly Arg Asp Gly>
 _a_a_ TRANSLATION OF HCVSEND.SEQ (RITS) [A]_a_a_a_>

640 650 660 670

TCC TGT CTC CCC GTG GCT CTC GGC CTA CCT GGG GCC CCA CAG ACC CCC
 AGG ACA GAG GGG CAC CGA GAG CCG GAT CGA CCC CGG GGT GTC TGG GGG
 Ser Cys Leu Pro Val Ala Leu Gly Leu Ala Gly Ala Pro Gln Thr Pro>
 _a_a_ TRANSLATION OF HCVSEND.SEQ (RITS) [A]_a_a_a_>

680 690 700 710 720

GGC GTA GGT CGC GCA ATT TGG GTA AGG TCA TCG ATA CCT TTA CGT GCG
 CCG CAT CCA GCG CGT TAA ACC CAT TCC AGT AGC TAT GGG AAT GCA CGC
 Gly Val Gly Arg Ala Ile Trp Val Arg Ser Ser Ile Pro Leu Arg Ala>
 _a_a_ TRANSLATION OF HCVSEND.SEQ (RITS) [A]_a_a_a_>

730 740 750 760 770

GCT TCG CCG ACC TCA TGG GGT ACA TAC CGC TCG TCG GCG CCC CTC TTG
 CGA AGC GGC TGG AGT ACC CCA TGT ATG GCG AGC AGC CGC GGG GAG AAC
 Ala Ser Pro Thr Ser Trp Gly Thr Tyr Arg Ser Ser Ala Pro Leu Leu>
 _a_a_ TRANSLATION OF HCVSEND.SEQ (RITS) [A]_a_a_a_>

780

790

800

810

820

GAG GCG CTG CCA GGG CCC TGG CGC ATG GCG TCC GGG TTC TGG AAG ACG
CTC CGC GAC GGT CCC GGG ACC GCG TAC CGC AGG CCC AAG ACC TTC TGC
Glu Ala Leu Pro Gly Pro Trp Arg Met Ala Ser Gly Phe Trp Lys Thr>
—a—a— TRANSLATION OF ECVSEND. SEQ (RITSA) [A]—a—a—a—>

830

840

GCG TGA ACT ATG CAA CAG
CGC ACT TGA TAC GTT GTC
Ala *** Thr Met Gln Gln>
— TRANSLATION OF H —>

FIGURE 12
(cont.)

Translation of HCV E1 SEQ (Rit Annotated Sequence)

Sequence Range: 1 to 166

10	20	30	40	50	60
*	*	*	*	*	*
*ARILNLKKK TNVTPTVAHR TSSSRVAVRS LVEFTCCRAG ALDWVCARRE RLPSGRNLEV					
70	80	90	100	110	120
*	*	*	*	*	*
DVSLSPRLVG PRAGPGLSPG TLGPSMAKRA AGGERDGSCLP VALGLAGAPQ TPGVGRAIHWV					
130	140	150	160		
*	*	*	*	*	*
RSSIPLRAAS PTSWGTYRSS APLLEALPGP WRMASGFWK A*TMQQ					

FIGURE 13